

OIEP

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/880,503

DATE: 06/28/2001  
 TIME: 14:56:06

# 2

Input Set : A:\9596-331.app  
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3 <110> APPLICANT: CINES, Douglas B  
 4 HIGAZI, Abd Al-Roof  
 6 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND  
 7 TISSUE CONTRACTABILITY  
 9 <130> FILE REFERENCE: 9596-331  
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/880,503  
 C--> 12 <141> CURRENT FILING DATE: 2001-06-13  
 14 <150> PRIOR APPLICATION NUMBER: US 60/212,847  
 15 <151> PRIOR FILING DATE: 2000-06-20  
 17 <160> NUMBER OF SEQ ID NOS: 18  
 19 <170> SOFTWARE: PatentIn Ver. 2.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 88  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Homo sapiens  
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 30 Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val  
 31 20 25 30  
 33 Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly  
 34 35 40 45  
 36 Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro  
 37 50 55 60  
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 40 65 70 75 80  
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 43 85  
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 47 <211> LENGTH: 47  
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 49 <213> ORGANISM: Homo sapiens  
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 55 Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn  
 56 20 25 30  
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 59 35 40 45  
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 63 <211> LENGTH: 411  
 64 <212> TYPE: PRT  
 65 <213> ORGANISM: Homo sapiens  
 67 <400> SEQUENCE: 3  
 68 Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly  
 69 1 5 10 15  
 71 Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn

ENTERED

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72          20          25          30
74 Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
75          35          40          45
77 Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
78          50          55          60
80 Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
81 65          70          75          80
83 Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
84          85          90          95
86 Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
87          100          105          110
89 Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
90          115          120          125
92 His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
93          130          135          140
95 Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
96 145          150          155          160
98 Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
99          165          170          175
101 Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
102          180          185          190
104 Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
105          195          200          205
107 Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
108          210          215          220
110 Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
111 225          230          235          240
113 Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
114          245          250          255
116 Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
117          260          265          270
119 Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
120          275          280          285
122 Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
123          290          295          300
125 Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
126 305          310          315          320
128 Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
129          325          330          335
131 Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
132          340          345          350
134 Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
135          355          360          365
137 Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
138          370          375          380
140 Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
141 385          390          395          400
143 Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
144          405          410

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147 <210> SEQ ID NO: 4
148 <211> LENGTH: 135
149 <212> TYPE: PRT
150 <213> ORGANISM: Homo sapiens
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156 Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
157 20 25 30
159 Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
160 35 40 45
162 Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
163 50 55 60
165 Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
166 65 70 75 80
168 Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
169 85 90 95
171 Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
172 100 105 110
174 Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
175 115 120 125
177 His Asp Cys Ala Asp Gly Lys
178 130 135
181 <210> SEQ ID NO: 5
182 <211> LENGTH: 276
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 5
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188 1 5 10 15
190 Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile
191 20 25 30
193 Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly
194 35 40 45
196 Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val
197 50 55 60
199 Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr
200 65 70 75 80
202 Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu
203 85 90 95
205 Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala
206 100 105 110
208 Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser
209 115 120 125
211 Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys
212 130 135 140
214 Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile
215 145 150 155 160
217 Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln

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218                               165                               170                               175
220 Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln
221                               180                               185                               190
223 Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala
224                               195                               200                               205
226 Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
227                               210                               215                               220
229 Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser
230                               225                               230                               235                               240
232 Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg
233                               245                               250                               255
235 Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn
236                               260                               265                               270
238 Gly Leu Ala Leu
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244 <212> TYPE: PRT
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249 1 5 10 15
251 Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
252 20 25 30
254 Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
255 35 40 45
257 Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
258 50 55 60
260 Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
261 65 70 75 80
263 Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
264 85 90 95
266 Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
267 100 105 110
269 Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
270 115 120 125
272 His Asp Cys Ala Asp Gly Lys Leu Lys Phe Gln Cys Gly Gln Lys Thr
273 130 135 140
275 Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu
276 145 150 155 160
278 Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser
279 165 170 175
281 Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile
282 180 185 190
284 Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile
285 195 200 205
287 Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met
288 210 215 220
290 Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp

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291 225                230                235                240
293 Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys
294                245                250                255
296 Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu
297                260                265                270
299 Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr
300                275                280                285
302 Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu
303                290                295                300
305 Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro
306 305                310                315                320
308 His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp
309                325                330                335
311 Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu
312                340                345                350
314 Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp
315                355                360                365
317 Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val
318                370                375                380
320 Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly
321 385                390                395                400
323 Leu Ala Leu
327 <210> SEQ ID NO: 7
328 <211> LENGTH: 323
329 <212> TYPE: PRT
330 <213> ORGANISM: Homo sapiens
332 <400> SEQUENCE: 7
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337 20 25 30
339 Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
340 35 40 45
342 Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr
343 50 55 60
345 Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu
346 65 70 75 80
348 Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser
349 85 90 95
351 Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile
352 100 105 110
354 Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile
355 115 120 125
357 Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met
358 130 135 140
360 Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp
361 145 150 155 160
363 Thr Leu Ala His His Asn Asp Ile Ala Leu Lys Ile Arg Ser Lys
364 165 170 175

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/880,503

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Input Set : A:\9596-331.app

Output Set: N:\CRF3\06282001\I880503.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date